

## Sequence Listing

<110> Flores, Heather Lin, Tanya P. Pai, Roger Shahrokh, Zahra Matthews, Timothy C. <120> Apo-2 LIGAND/TRAIL FORMULATIONS <130> P1857R1P1 <140> US 10/771,254 <141> 2004-02-03 <150> US 60/338,249 <151> 2001-11-13 <150> PCT/US02/36251 <151> 2002-11-12 <160> 2 <210> 1 <211> 281 <212> PRT <213> Homo sapiens <400> 1 Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys 20 Val Ala Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu 50 Asp Asp Ser Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser 65 Pro Cys Trp Gln Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu

Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr

125 130 135

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys 140 145 Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser 155 160 Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly 170 175 Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu 185 190 195 Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile 200 205 Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr 230 235 Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg 250 Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His 260 265 270 Glu Ala Ser Phe Phe Gly. Ala Phe Leu Val Gly 275

<210> 2

<211> 1042

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 447

<223> unknown base

## <400> 2

tttcctcact gactataaaa gaatagagaa ggaagggctt cagtgaccgg 50 ctgcctggct gacttacagc agtcagactc tgacaggatc atggctatga 100 tggaggtcca ggggggaccc agcctgggac agacctgcgt gctgatcgtg 150 atcttcacag tgctcctgca gtctctctgt gtggctgtaa cttacgtgta 200 ctttaccaac gagctgaagc agatgcagga caagtactcc aaaagtggca 250 ttgcttgtt cttaaaagaa gatgacagtt attgggaccc caatgacgaa 300 gagagtatga acagccctg ctggcaagtc aagtggcaac tccgtcagct 350

egetagaaag atgatttga gaacetetga ggaaaccatt tetacagtte 400
aagaaaaagca acaaaatatt teteceetag tgagagaaag aggteeneag 450
agagtagcag eteacataac tgggaccaga ggaaagaagca acacattgte 500
tteeteeaaac teeaagaatg aaaaggetet gggeegeaaa ataaacteet 550
gggaatcate aaggagtggg catteattee tgageaacet geacttgagg 600
aatggtgaac tggteateea tgaaaaaaggg ttttactaca teetatteeea 650
aacatacttt egattteagg aggaaataaa agaaaacaca aagaacgaca 700
aacaaatggt eeaatatat tacaaataca eaagttatee tgaceetata 750
ttgttgatga aaagtgetag aaatagttgt tggtetaaag atgeagaata 800
tggactetat teeatetate aagggggaat atttgagett aaggaaaatg 850
acagaatttt tgtttetgta acaaatgage acttgataga catggaccat 900
gaagecagtt ttttegggge etttttagtt ggetaactga eetggaaaga 950
aaaaagcaata aceteaaagt gaetatteag tttteaggat gatacactat 1000
gaagatgttt caaaaaatet gaecaaaaca aacaaacaga aa 1042